Supplementary Table 1. *DYRK1A* variants detected in 892 ASD/ID/DD samples

DYRK1A Exon/ Intron (domain)	Genome Position（Chr21）	Nucleotide Change	Amnio Acid Change	dbSNP ID	Variant Type	Detected in Patients			MAF in Patients	MAF in Controls		Allele Frequency				Function Prediction				Splicing predict		
						hetero	homo	patients			ExAc	1000 Genomes	NHLBI ESP Total	NHLBI ESP Africa	NHLBI ESP European	SIFT prediction	Polyphen prediction	MutationTaster	Conservation PhyloP p-value	MaxEnt	NNSPLICE	HSF
7	38858865	c.613C>T	p.R205X		nonsense	1	0	341	0.00158	0	0/~60000	0/~1000	0/~6500			possibly damaging	Deleterious (score: 0, median: 3.92)	disease causing (p-value: 1)	N/A			
8	38862527	c.715G>T	p.E239X		nonsense	1	0	315	0.00158	0	0/~60000	0/~1000	0/~6500			possibly damaging	Deleterious (score: 0, median: 3.92)	disease causing (p-value: 1)	N/A			
6	38852988	c.376G>T	p.D126Y		missense	1	0	332	0.00151	0	0/~60000	0/~1000	0/~6500			possibly damaging	Deleterious (score: 0, median: 4.32)	disease causing (p-value: 1)	Highly conserved nucleotide (phyloP: 5.86 [-14.1;6.4]			
6	38853010	c.398G>A	p.R133Q		missense	1	0	332	0.00151	0	0/~60000	0/~1000	0/~6500			possibly damaging	Deleterious (score: 0, median: 4.32)	disease causing (p-value: 1)	Moderately conserved nucleotide (phyloP: 3.11 [-14.1;6.4])			
8	38862589	c.777G>T	p.L259F		missense	1	0	315	0.00158	0	0/~60000	0/~1000	0/~6500			possibly damaging	Deleterious (score: 0, median: 3.92)	disease causing (p-value: 1)	Highly conserved nucleotide (phyloP: 6.02 [-14.1;6.4])			
11	38877719	c.1373G>T	p.R458M		missense	1	0	360	0.00138	0	0/~60000	0/~1000	0/~6500			possibly damaging	Deleterious (score: 0.02, median: 3.93)	disease causing (p-value: 1)	Highly conserved nucleotide (phyloP: 6.02 [-14.1;6.4])			
11	38877803	c.1457G>GA	p.G486D		missense	1	0	360	0.00138	0	0/~60000	0/~1000	0/~6500			possibly damaging	Deleterious (score: 0.01, median: 3.93)	disease causing (p-value: 1)	Highly conserved nucleotide (phyloP: 6.02 [-14.1;6.4])			
6	38852967	c.355C>T	p.H119Y		missense	1	0	332	0.00151	0	0/~60000	0/~1000	0/~6500			possibly damaging	Tolerated (score: 0.14, median: 4.32)	disease causing (p-value: 1)	Highly conserved nucleotide (phyloP: 6.18 [-14.1;6.4])			
7	38858835	c.583G>A	p.A195T		missense	1	0	341	0.00146	0	0/~60000	0/~1000	0/~6500			possibly damaging	Tolerated (score: 0.09, median: 3.93)	disease causing (p-value: 1)	Weakly conserved nucleotide (phyloP: 1.58 [-14.1;6.4])			
4	38845158	c.183G>C	p.Q61H		missense	1	0	337	0.00148	0	0/~60000	0/~1000	0/~6500			benign	Tolerated (score: 0.15, median: 4.32)	disease causing (p-value: 1)	Highly conserved nucleotide (phyloP: 6.26 [-14.1;6.4])			
6	38853080	c.468G>A	p.M156I		missense	1	0	332	0.00151	0	0/~60000	0/~1000	0/~6500			benign	Tolerated (score: 0.06, median: 4.32)	disease causing (p-value: 1)	Highly conserved nucleotide (phyloP: 6.26 [-14.1;6.4])			
3	38845144	c.169 T>C	p.S57P	rs1049763	missense	1	0	373	0.00134	0.00011	0.00004969	0/~1000	0/~6500			benign	Tolerated (score: 0.14, median: 4.32)	polymorphism (p-value: 0.997)	Not conserved nucleotide (phyloP: -0.12 [-14.1;6.4])			
4	38845173	c.198A>G	p.L66L		coding-synonymous	1	0	337			0/~60000	0/~1000		none	G=1/A=13005	unknown						
5	38850536	c.261C>T	p.D87D	rs1049764	coding-synonymous	2	0	347			0/~60000	0/~1000		T=6/C=13000	T=6/C=13000	unknown						
6	38852972	c.360A>G	p.Q120Q		coding-synonymous	1	0	332			0/~60000	0/~1000		none	G=1/A=13005	unknown						
6	38862547	c.735 C>T	p.L245L		coding-synonymous	1	0	368			0/~60000	0/~1000	0/~6500			unknown						
6	38862685	c.873 A>G	p.Glu291Glu		coding-synonymous	1	0	368			0/~60000	0/~1000	0/~6500			unknown						
11	38877681	c.1335G>A	p.T445T		coding-synonymous	1	0	360			0/~60000	0/~1000		none	A=1/G=13005	unknown						
11	38877762	c.1416T>C	p.Y472Y	rs55854596	coding-synonymous	4	0	360	0.00555	0.00023	0.006861; 0.009/19	T=0.9934/C=0.0066		C=62/T=12944	C=62/T=12944	unknown						
11	38877861	c.1515G>T	p.S505S		coding-synonymous	1	0	360			0/~60000	0/~1000	0/~6500			unknown						
11	38884651	c.2109 C>T	p.Thr703Thr		coding-synonymous	1	0	395			0/~60000	0/~1000	0/~6500			unknown						
												0/~1000										
3	38792696	c.10+10G>T			intron	1	0	1/362			0/~60000	0/~1000	0/~6500									
3	38792739	c.10+53C>A			intron	0	1	362				0/~1000	0/~6500									
3	38792749	c.10+63T>C			intron	1	0	362				0/~1000	0/~6500									
3	38792790	c.10+104_10+106 delGGG			intron	69	6	362			??	0/~1000	0/~6500									
3	38792824	c.10+138G>T			intron	0	0	362			??	0/~1000	0/~6500									
4	38844760	c.11-226T>A			intron	73	9	337				T=0.9413/A=0.0587	0/~6500									
4	38844811	c.11-175C>T			intron	18	4	337				C=0.9315/T=0.0685	0/~6500									
4	38844827	c.11-159A>G			intron	1	0	337				0/~1000	0/~6500									
4	38844926	c.11-60C>A			intron	1	0	337				0/~1000	0/~6500									
5	38850470	c.208-13C>G		rs140466090	intron	2	0	347			0.003402; 0.002/5	C=0.9978/G=0.0022		G=52/C=12954	G=52/C=12954					-6.10%	-30.20%	0.00%
6	38852699	c.328-241C>G			intron	1	0	332				0/~1000	0/~6500									
6	38852728	c.328-212G>A			intron	67	9	332				G=0.8838/A=0.1162	0/~6500									
6	38852793	c.328-147G>A			intron	1	0	332				0/~1000	0/~6500									
6	38852846	c.328-94C>G			intron	1	0	332				0/~1000	0/~6500									
6	38852869	c.328-71A>G			intron	1	0	332				0/~1000	0/~6500									
6	38852905	c.328-35A>T			intron	1	0	332				0/~1000	0/~6500									
6	38852927	c.328-13_328-12insATA			intron	1	0	332			0/~60000	0/~1000	0/~6500							-7.90%	-1.60%	0.00%
6	38853213	c.516+85G>C			intron	1	0	332				G=0.9990/C=0.0010	0/~6500									
7	38858597	c.517-172G>A			intron	1	0	341				0/~1000	0/~6500									
7	38858628	c.517-141C>A			intron	1	0	341				0/~1000	0/~6500									
7	38858640	c.517-129_517-126 delAAGG			intron	1	0	341				0/~1000	0/~6500									
7	38858655	c.517-114A>C			intron	1	0	341				A=0.9996/C=0.0004	0/~6500									
7	38858658	c.517-111 delA			intron	4	0	341				0/~1000	0/~6500									
7	38858938	c.664+22G>A		rs55650427	intron	111	21	341				G=0.8087/A=0.1913		A=2256/G=10744	A=2256/G=10744							
7	38859017	c.664+101G>A			intron	1	0	341				G=0.9994/A=0.0006	0/~6500									
8	38862373	c.665-104T>A			intron	129	79	315				T=0.5601/A=0.4399	0/~6500									
10	38868591	c.1239+31T>G		rs79423895	intron	1	0	350				T=0.9984/G=0.0016		G=28/T=12976	G=28/T=12976							
11	38877503	c.1240-83T>G			intron	49	7	360				T=0.9235/G=0.0765	0/~6500									
11	38877544	c.1240-42T>G			intron	3	0	360				T=0.9956/G=0.0044		G=32/T=12974	G=32/T=12974							
11	38877579	c.1240-7C>T			intron	1	0	360				C=0.9984/T=0.0016		T=10/C=12996	none					-5.60%	0.40%	-0.40%
1	38792661	c.-16 G>A			intron	1	0	411				G=0.9980/A=0.0020	0/~6500									
2	38845294	c.207+112 G>A		rs2898316	intron	4	0	373				G=0.9599/A=0.0401	0/~6500									
5	38858938	c.664+22 G>A		rs55650427	intron	126	0	433				G=0.8087/A=0.1913		A=2256/G=10744	A=2256/G=10744							
7	38865507	c.1098+42 C>G		rs2835772	intron	241	0	431				C=0.6496/G=0.3504		G=3954/C=9052	G=3954/C=9052							
13	38884613	c.1755+6003G>T			3'UTR	1	0	309				0/~1000	0/~6500									

Supplementary Table 2 variants found in *DYRK1A* correspondence to *Dyrk1A*

Exon	Nucleotide Change	AA code	Protein Change	Polyphen prediction	Domain
3	c.183G>C	CAG>CAC	p.Q61H	benign	
5	c.355C>T	CAC>TAC	p.H119Y	possibly damaging	
5	c.376G>T	GAT>TAT	p.D126Y	possibly damaging	Biopartite nuclear localization
5	c.398G>A	CGG>CAG	p.R133Q	possibly damaging	signal （117-134）
5	c.468G>A	ATG>ATA	p.M156I	benign	
6	c.583G>A	GCG>ACG	p.A195T	possibly damaging	protein kinase（159-479）
6	c.613C>T	CGG>TGA	p.R205X		protein kinase
7	c.715G>T	GAA>TAA	p.E239X		protein kinase
7	c.777G>T	TTG>TTT	p.L259F	possibly damaging	protein kinase
10	c.1373G>T	AGG>ATG	p.R458M	possibly damaging	protein kinase
10	c.1457G>GA	GGT>GAT	p.G486D	possibly damaging	protein kinase

Supplementary Table 3 primers for mutagenesis analysis

Primer No.	the Specific Sequence
Dyrk1A_H119Y-F	TACCAACAGGGCCAGGGGGACGATT
Dyrk1A_H119Y-R	TCTTCGCTTCTTTTTTGCATAGTAAACC
Dyrk1A_D126Y-F	TATTCCAGTCATAAGAAGGAGCGGA
Dyrk1A_D126Y-R	GTCCCCCTGGCCCTGTTGGTGTCTT
Dyrk1A_R133Q-F	AGAAGGTTTACAATGATGGTTACGATG
Dyrk1A_R133Q-R	GCTCCTTCTTATGACTGGAATCGTC
Dyrk1A_A195T-F	ACGTTTCTGAATCAAGCCCAGATAG
Dyrk1A_A195T-R	TTTCTTGTTCTTGATGATTTTAATGGCG
Dyrk1A_R205X-F	TGGCTGCTTGAGCTCATGAACAAAC
Dyrk1A_R205X-R	CACTTCTATCTGGGCTTGATTCAG
Dyrk1A_E239X-F	TAAATGCTGTCCTATAATCTCTATG
Dyrk1A_E239X-R	AAACACTAAACAGAGATGGTTTCGAAAC
Dyrk1A_L259F-F	TAACCTAACACGAAAGTTTGCGCAAC
Dyrk1A_L259F-R	AAAGAGACCCCTCGGAAGTTGGTGTTTC
Dyrk1A_R458M-F	TGATGCTTGATTATGACCCCAAAAC
Dyrk1A_R458M-R	TTAAAATGAGGTCTTTGAACTTCAAGTAG
Dyrk1A_G486D-F	ATACCAACACAAGTAACAGTGTGTC
Dyrk1A_G486D-R	CTTCATCAGCTGTTTTCTTGAAAAAAC

Supplementary figure 1. Dang et al.